

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/232436 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length  
Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>  
Sequence(s) 11 missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

## RAW SEQUENCE LISTING

DATE: 09/13/2001

PATENT APPLICATION: US/09/732,436A

TIME: 15:39:05

Input Set : A:\Cura-611.app

Output Set: N:\CRF3\09132001\I732436A.raw

pg 5-6

3 <110> APPLICANT: Prayaga, Sudhirdas  
 4 Shimkets, Richard  
 6 <120> TITLE OF INVENTION: NOVEL INTERFERON OMEGA AND NUCLEIC ACIDS ENCODING SAME  
 8 <130> FILE REFERENCE: 15966-615  
 10 <140> CURRENT APPLICATION NUMBER: 09/732,436A  
 C--> 11 <141> CURRENT FILING DATE: 1999-07-12  
 13 <150> PRIOR APPLICATION NUMBER: 60/169,887  
 14 <151> PRIOR FILING DATE: 1999-12-09  
 16 <150> PRIOR APPLICATION NUMBER: 60/170,230  
 17 <151> PRIOR FILING DATE: 1999-12-10  
 19 <160> NUMBER OF SEQ ID NOS: 22  
 21 <170> SOFTWARE: PatentIn Ver. 2.1  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 475  
 25 <212> TYPE: PRT  
 26 <213> ORGANISM: Artificial Sequence  
 28 <220> FEATURE:  
 29 <223> OTHER INFORMATION: Description of Artificial Sequence: Curagen clone  
 30 AC015663\_A  
 32 <400> SEQUENCE: 1  
 33 Ala Cys Cys Ala Ala Thr Gly Gly Thr Cys Thr Cys Cys Thr Thr Gly  
 34 1 5 10 15  
 36 Cys Thr Gly Gly Thr Gly Gly Cys Ala Thr Thr Gly Gly Thr Gly Ala  
 37 20 25 30  
 39 Thr Gly Ala Thr Cys Thr Cys Cys Thr Gly Cys Cys Ala Cys Ala Thr  
 40 35 40 45  
 42 Cys Thr Ala Thr Thr Cys Cys Cys Thr Thr Thr Thr Cys Thr Gly Cys  
 43 50 55 60  
 45 Gly Ala Cys Cys Thr Gly Cys Cys Thr Ala Ala Ala Gly Cys Thr Cys  
 46 65 70 75 80  
 48 Ala Gly Gly Thr Gly Ala Thr Thr Thr Cys Thr Gly Cys Cys Cys Thr  
 49 85 90 95  
 51 Cys Cys Ala Thr Ala Ala Gly Ala Thr Gly Cys Ala Cys Cys Ala Gly  
 52 100 105 110  
 54 Cys Ala Gly Ala Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr  
 55 115 120 125  
 57 Thr Thr Thr Thr Ala Cys Ala Cys Ala Ala Gly Gly Gly Cys Thr Thr  
 58 130 135 140  
 60 Gly Thr Cys Thr Gly Ala Thr Gly Cys Thr Thr Gly Gly Ala Ala Thr  
 61 145 150 155 160  
 63 Ala Gly Gly Gly Cys Cys Thr Thr Cys Cys Thr Gly Gly Ala Cys Ala  
 64 165 170 175  
 66 Ala Ala Cys Thr Cys Cys Ala Gly Ala Cys Thr Gly Gly Ala Thr Thr  
 67 180 185 190  
 69 Thr Cys Ala Thr Cys Ala Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala  
 70 195 200 205  
 72 Gly Ala Cys Cys Thr Gly Gly Ala Gly Ala Cys Cys Thr Gly Cys Thr

Does Not Comply  
Corrected Diskette Needed

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73      210      215      220
75 Thr Thr Gly Gly Thr Ala Thr Ala Gly Ala Gly Gly Ala Thr Gly Gly
76 225      230      235      240
78 Gly Ala Ala Gly Cys Ala Ala Gly Ala Gly Thr Cys Thr Gly Cys Cys
79      245      250      255
81 Cys Thr Gly Gly Ala Ala Ala Thr Thr Gly Ala Gly Gly Gly Cys Cys
82      260      265      270
84 Cys Thr Ala Cys Ala Cys Thr Gly Gly Cys Cys Ala Thr Ala Ala Ala
85      275      280      285
87 Gly Ala Gly Gly Thr Ala Cys Thr Thr Cys Cys Ala Gly Gly Gly Ala
88      290      295      300
90 Gly Thr Ala Cys Ala Thr Thr Thr Cys Thr Thr Cys Thr Thr Gly Ala
91 305      310      315      320
93 Ala Ala Gly Ala Gly Ala Gly Gly Ala Ala Ala Thr Thr Cys Ala Gly
94      325      330      335
96 Gly Ala Ala Cys Thr Gly Thr Ala Cys Cys Thr Gly Gly Gly Ala Gly
97      340      345      350
99 Gly Thr Thr Gly Thr Cys Gly Thr Ala Ala Thr Gly Gly Thr Ala Ala
100      355      360      365
102 Ala Gly Gly Gly Ala Thr Thr Thr Thr Thr Cys Thr Thr Ala Ala Gly
103      370      375      380
105 Cys Ala Cys Ala Ala Ala Ala Cys Thr Thr Cys Ala Ala Gly Ala Ala
106 385      390      395      400
108 Ala Ala Ala Gly Ala Gly Ala Ala Cys Ala Gly Ala Ala Gly Ala Ala
109      405      410      415
111 Ala Ala Gly Ala Gly Ala Ala Cys Thr Gly Cys Ala Ala Ala Ala Ala
112      420      425      430
114 Ala Ala Ala Thr Cys Thr Gly Gly Ala Ala Ala Ala Gly Gly Thr Ala
115      435      440      445
117 Ala Thr Cys Thr Ala Thr Thr Thr Ala Gly Cys Ala Gly Ala Ala Gly
118      450      455      460
120 Ala Gly Thr Gly Ala Ala Ala Gly Cys Thr Gly
121 465      470      475
124 <210> SEQ ID NO: 2
125 <211> LENGTH: 610
126 <212> TYPE: PRT
127 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Description of Artificial Sequence: Curagen clone
132 <400> SEQUENCE: 2
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134 1      5      10      15
136 Cys Thr Gly Gly Thr Gly Gly Cys Ala Thr Thr Gly Gly Thr Gly Ala
137      20      25      30
139 Thr Gly Ala Thr Cys Thr Cys Cys Thr Gly Cys Cys Ala Cys Ala Thr
140      35      40      45
142 Cys Thr Ala Thr Thr Cys Cys Cys Thr Thr Thr Thr Thr Cys Thr Gly Cys
143      50      55      60
145 Gly Ala Cys Cys Thr Gly Cys Cys Thr Asn Asn Asn Asn Asn Asn Asn

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146 65              70              75              80
148 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
149              85              90              95
151 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
152              100             105             110
154 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
155              115             120             125
157 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
158              130             135             140
160 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
161 145             150             155             160
163 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
164              165             170             175
166 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
167              180             185             190
169 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
170              195             200             205
172 Ala Ala Ala Gly Cys Thr Cys Ala Gly Gly Thr Gly Ala Thr Thr Thr
173              210             215             220
175 Cys Thr Gly Cys Cys Cys Thr Cys Cys Ala Thr Ala Ala Gly Ala Thr
176 225             230             235             240
178 Gly Cys Ala Cys Cys Ala Gly Cys Ala Gly Ala Thr Cys Thr Thr Cys
179              245             250             255
181 Ala Gly Cys Cys Thr Cys Thr Thr Thr Thr Thr Ala Cys Ala Cys Ala
182              260             265             270
184 Ala Gly Gly Gly Cys Thr Thr Gly Thr Cys Thr Gly Ala Thr Gly Cys
185              275             280             285
187 Thr Thr Gly Gly Ala Ala Thr Ala Gly Gly Gly Cys Cys Thr Thr Cys
188              290             295             300
190 Cys Thr Gly Gly Ala Cys Ala Ala Ala Cys Thr Cys Cys Ala Gly Ala
191 305             310             315             320
193 Cys Thr Gly Gly Ala Thr Thr Thr Cys Ala Thr Cys Ala Gly Cys Ala
194              325             330             335
196 Gly Cys Thr Gly Gly Ala Ala Gly Ala Cys Cys Thr Gly Gly Ala Gly
197              340             345             350
199 Ala Cys Cys Thr Gly Cys Thr Thr Thr Gly Gly Thr Ala Thr Ala Gly
200              355             360             365
202 Ala Gly Gly Ala Thr Gly Gly Gly Ala Ala Gly Cys Ala Ala Gly Ala
203              370             375             380
205 Gly Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly Ala Ala Ala Thr Thr
206 385             390             395             400
208 Gly Ala Gly Gly Gly Cys Cys Cys Thr Ala Cys Ala Cys Thr Gly Gly
209              405             410             415
211 Cys Cys Ala Thr Ala Ala Ala Gly Ala Gly Gly Thr Ala Cys Thr Thr
212              420             425             430
214 Cys Cys Ala Gly Gly Gly Ala Gly Thr Ala Cys Ala Thr Thr Thr Cys
215              435             440             445
217 Thr Thr Cys Thr Thr Gly Ala Ala Ala Gly Ala Gly Ala Gly Gly Ala
218              450             455             460

```

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220 Ala Ala Thr Thr Cys Ala Gly Gly Ala Ala Cys Thr Gly Thr Ala Cys
221 465                               470                               475                               480
223 Cys Thr Gly Gly Gly Ala Gly Gly Thr Thr Gly Thr Cys Gly Thr Ala
224                               485                               490                               495
226 Ala Thr Gly Gly Thr Ala Ala Ala Gly Gly Gly Ala Thr Thr Thr
227                               500                               505                               510
229 Thr Cys Thr Thr Ala Ala Gly Cys Ala Cys Ala Ala Ala Cys Thr
230                               515                               520                               525
232 Thr Cys Ala Ala Gly Ala Ala Ala Ala Gly Ala Gly Ala Ala Cys
233                               530                               535                               540
235 Ala Gly Ala Ala Gly Ala Ala Ala Ala Gly Ala Gly Ala Ala Cys Thr
236 545                               550                               555                               560
238 Gly Cys Ala Ala Ala Ala Ala Ala Ala Ala Thr Cys Thr Gly Gly Ala
239                               565                               570                               575
241 Ala Ala Ala Gly Gly Thr Ala Ala Thr Cys Thr Ala Thr Thr Thr Ala
242                               580                               585                               590
244 Gly Cys Ala Gly Ala Ala Gly Ala Gly Thr Gly Ala Ala Ala Gly Cys
245                               595                               600                               605
247 Thr Gly
248 610
251 <210> SEQ ID NO: 3
252 <211> LENGTH: 1887
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Description of Artificial Sequence: Curagen clone
258 AF038458_A
260 <400> SEQUENCE: 3
261 atggccatcc tcccgttgct cctgtgcctg ctgccgctgg cccctgcctc atccccaccc 60
262 cagtcagcca caccagccc atgtccccgc cgctgccgct gccagacaca gtcgctgccc 120
263 ctaagcgtgc tgtgcccagg ggcaggcctc ctgttcgtgc caccctcgct ggaccgccc 180
264 gcagccgagc tgcggctggc agacaaactt atcgccctcg tgcgcccggc cgacctggcc 240
265 aacatgacag gcctgctgca tctgagcctg tcgcggaaca ccatccgcca cgtggctgcc 300
266 ggcgcccttc ccgacctgcg ggccctgcgt gccctgcacc tggatggcaa ccggctgacc 360
267 tactggggcg agggccagct gcgcggcctg gtcaacttgc gccacctcat cctcagcaac 420
268 aaccagctgg cagcgtggc ggccggcgcc ctggatgatt gtgccgagac actggaggac 480
269 ctcgacctct cctacaacaa cctcgagcag ctgccctggg aggccctggg ccgcctgggc 540
270 aacgtcaaca cgttgggcct cgaccacaac ctgctggctt ctgtgcccgc cggcgctttt 600
271 tcccgctgc acaagctggc ccgctgggac atgacctcca accgcctgac cacaatccca 660
272 cccgacccac tcttctcccg cctgcccctg ctgcgccagg cccggggctc gcccgctct 720
273 gccctggctg tggcctttgg cgggaacccc ctgcaactga actgcgagct ggtgtggctg 780
274 cgtcgctgg cgcgggagga cgacctcgag gcctgcgcgt cccacactgc tctgggcggc 840
275 cgctacttct gggcggtggg cgaggaggag tttgtctgcg agccgcccgt ggtgactcac 900
276 cgctcaccac ctctggctgt gcccgagggt cggccggctg cctgcgctg ccgggcagt 960
277 ggggacccag agccccgtgt gcgttgggtg tcaccccagg gccggctgct aggcaactca 1020
278 agccgtgccc gcgccttccc caatgggacg ctggagctgc tggtcaccga gccgggtgat 1080
279 ggtggcatct tcacctgat tgcggccaat gcagctggcg aggccacagc tgctgtggag 1140
280 ctgactgtgg gtccccacc acctcctcag ctagccaaca gcaccagctg tgaccccccg 1200
281 cgggacgggg atcctgatgc tctcacccca cctccgctg cctctgcttc tgccaagggt 1260

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DATE: 09/13/2001

PATENT APPLICATION: US/09/732,436A

TIME: 15:39:05

Input Set : A:\Cura-611.app

Output Set: N:\CRF3\09132001\I732436A.raw

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282 gccgacactg ggccccctac cgaccgtggc gtccaggtga ctgagcacgg ggccacagct 1320
283 gctcttgtcc agtggccgga tcagcggcct atcccgggca tccgcatgta ccagatccag 1380
284 tacaacagct cggctgatga catcctcgtc tacaggatga tcccggcgga gagccgctcg 1440
285 ttctgtctga cggacctggc gtcaggccgg acctacgata tgtgcgtgct cgccgtgtat 1500
286 gaggacagcg ccacggggct cacggccaag cggcctgtgg gctgcgcccg cttctccacc 1560
287 gaacctgccc tgcggccatg cggggcgccg cacgctccct tcctgggcgg cagcatgata 1620
288 atcgcgctgg gcggcgctcat cgtagcctcg gtactggtct tcattctcgt gctgctaata 1680
289 cgctacaagg tgcacggcgg ccagccccc ggcaaggcca agattcccgc gctgttagc 1740
290 agcgtttgct cccagaccaa cggcgccctg ggccccacgc ccacgcccgc cccgcccgc 1800
291 ccggagcccg cggcgctcag ggcccacacc gtggtccagc tggactgcga gccctggggg 1860
292 cccggccacg aacctgtggg accctag 1887
295 <210> SEQ ID NO: 4
296 <211> LENGTH: 365
297 <212> TYPE: PRT
298 <213> ORGANISM: Equus caballus
300 <400> SEQUENCE: 4
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302 1 5 10 15
304 Cys Gly Cys Gly Thr Cys Thr Gly Thr Cys Cys Thr Cys Cys Ala Cys
305 20 25 30
307 Gly Ala Gly Ala Thr Gly Cys Thr Cys Cys Ala Gly Cys Ala Gly Ala
308 35 40 45
310 Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr Thr Cys Cys Ala
311 50 55 60
313 Cys Ala Cys Ala Gly Ala Gly Cys Gly Cys Thr Cys Gly Thr Cys Thr
314 65 70 75 80
316 Gly Cys Thr Gly Cys Cys Thr Gly Gly Ala Ala Cys Ala Cys Gly Ala
317 85 90 95
319 Cys Cys Cys Thr Cys Cys Thr Gly Gly Ala Cys Gly Ala Ala Cys Thr
320 100 105 110
322 Cys Thr Gly Cys Ala Cys Gly Gly Gly Ala Cys Thr Cys Cys Thr Thr
323 115 120 125
325 Cys Gly Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala Gly Ala Cys Cys
326 130 135 140
328 Thr Gly Gly Ala Cys Ala Cys Cys Thr Gly Thr Thr Thr Gly Gly Ala
329 145 150 155 160
331 Gly Cys Ala Gly Gly Ala Gly Ala Thr Gly Gly Gly Ala Gly Ala Gly
332 165 170 175
334 Gly Ala Ala Gly Ala Ala Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly
335 180 185 190
337 Gly Ala Ala Cys Thr Gly Thr Gly Cys Gly Cys Cys Cys Thr Ala Cys
338 195 200 205
340 Ala Cys Thr Gly Gly Cys Cys Gly Thr Gly Ala Ala Gly Ala Gly Gly
341 210 215 220
343 Thr Ala Cys Thr Thr Cys Cys Gly Gly Gly Gly Ala Thr Cys Cys
344 225 230 235 240
346 Ala Thr Cys Thr Cys Thr Ala Cys Cys Thr Gly Ala Ala Ala Gly Ala
347 245 250 255
349 Gly Ala Ala Gly Ala Ala Ala Thr Ala Cys Ala Gly Thr Gly Ala Cys

```

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

09/732,436A 6

<210> 11

<211> 112

<212> PRT

<213> Unknown

see item 11 on Ena Summary Sheet

<400> 11

VERIFICATION SUMMARY

DATE: 09/13/2001

PATENT APPLICATION: US/09/732,436A

TIME: 15:39:06

Input Set : A:\Cura-611.app

Output Set: N:\CRF3\09132001\I732436A.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:626 M:258 W: Mandatory Feature missing, <220> FEATURE:

L:626 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: